

**Table S4. Non-engineered mutations identified in S-ExoN1 P1 c1.**

Mutation <sup>a</sup>	Codon change	Amino acid change <sup>b</sup>	Location
C 4382 T	G <u>C</u> C→G <u>T</u> C	Ala 555 Val	nsp 3
T 6494 A	G <u>T</u> G→G <u>A</u> G	Val 1259 Glu	nsp 3
T 17465 C	G <u>G</u> T→G <u>G</u> C	none	nsp 13
C 20288 T	G <u>G</u> C→G <u>G</u> T	none	nsp 15
C 25355 T	<u>C</u> AT→ <u>I</u> AT	His 30 Tyr	ORF 3a
C 29454 T	n.a.	n.a.	3' UTR

<sup>a</sup> The entire genome was sequenced except for the terminal 20 nt at each end.

<sup>b</sup> Amino acid positions in nsps refer to location within the respective mature nsp. 'None' indicates synonymous changes.